

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Philip E.Branton et al.

5 (ii) TITLE OF THE INVENTION: Adenovirus E4 Protein For  
Inducing Cell Death

(iii) NUMBER OF SEQUENCES: 4

## (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Clark & Elbing LLP
- (B) STREET: 176 Federal Street
- (C) CITY: Boston
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02110

## 10 (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

## 15 (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 3 July 1997
- (C) CLASSIFICATION:

## 20 (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/021,273
- (B) FILING DATE: 5 July 1996

## 25 (viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/028,740
- (B) FILING DATE: 22 October 1996

## 30 (ix) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Bieker-Brady, Kristina
- (B) REGISTRATION NUMBER: 39,109
- (C) REFERENCE/DOCKET NUMBER: 50013/002W01

## 35 (x) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-428-0200
- (B) TELEFAX: 617-428-7045
- (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 885 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGACTACGT	CGGGGTCTTC	ATTGGCATG	ACACTACGAC	CAACAGCAGTC	TCGGTTGTC	60
CGGGCACTC	COTACAGTAG	GAATGCTCTA	CCCTCTTCTT	AGACAAAGAA	CCGGCGTACCC	120
ATACTGGAGG	ATCATCCGGC	GCTGGCCCAA	TGTAACACTT	TGACAATGCA	CAACGTGAGT	180
TACGTGCGAG	GTCCTCCCTG	CAGTGTGGGA	TTAACCGCTA	TTCAGGAATG	GGTTGTTCCC	240
TGGGGATATGG	TTCTAACGCCG	GGAGGGACCTT	TAATCCCTGC	GGAACTGTAT	GCACGTGTC	300
CTGTGTTGTC	CCAAACATGTA	TATCATGCG	AGCATGATGA	TCTTGTGTTA	CGACTCTGG	360
GCTCTCACT	GTCATTGTT	CAGTCCCGT	TCCCTCGAGT	GTATAGCCG	CGGGCAGGTT	420
TTGGCCAGGT	GTTTTGGAGAT	GGTGGTGGAT	GGGGCCATCT	TTAACAGAG	GTTTTATATGG	480
TACGGGGAGG	TGGTGAATTA	CAACATGCC	AAAGGATGAA	TGTTTATGTC	CAGGCTGTTT	540
ATGAGGGGTC	GCCACTTAAT	CTACCTGCG	TTGGTGATG	ATGGCCACGT	GGGTTCTGTG	600
GTCCCCGCCA	TAAGCTTGG	TAACAGGCC	TCTGACTGTG	GGATTTTGA	CAATATTGTC	660
TCGTCTGTC	GCGACTTGT	TCTGTGATTA	ATGGATGATCA	GGGGTGGCTG	CTGTGGCCGG	720
AGGACAAGGC	GCCTTATGCT	GGGGCGGTG	CGAATCATG	CTGAGGAGAC	CACTGGCATG	780
TTGTATTCTCT	CGAGGGACCGA	GGGGCGGGCG	CGACAGCTTA	TTCCGGCGGT	GCTCGACGAC	840
CACCGGCTTA	TCTGTGATCA	CGATTATGAC	TCTACCCCCA	TGTAG		885

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 294 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Thr	Ser	Gly	Val	Pro	Phe	Gly	Met	Thr	Leu	Arg	Pro	Thr	Arg
1					5				10				15		
Ser	Arg	Leu	Ser	Arg	Arg	Thr	Pro	Tyr	Ser	Arg	Asp	Arg	Leu	Pro	Pro
					20				25			30			
Phe	Glu	Thr	Glu	Thr	Arg	Ala	Thr	Ile	Leu	Glu	Asp	His	Pro	Leu	Leu
					35				40			45			
Pro	Glu	Cys	Asn	Thr	Leu	Thr	Met	His	Asn	Val	Ser	Tyr	Val	Arg	Gly
					50				55			60			
Leu	Pro	Cys	Ser	Val	Gly	Phe	Thr	Leu	Ile	Gln	Glu	Trp	Val	Val	Pro
65					70				75			80			
Trp	Asp	Asp	Met	Val	Leu	Thr	Arg	Glu	Glu	Leu	Val	Ile	Leu	Arg	Cys
					85				90			95			
Met	His	Val	Cys	Leu	Cys	Cys	Ala	Asn	Ile	Asp	Ile	Met	Thr	Ser	Met
					100				105			110			
Met	Ile	His	Gly	Tyr	Glu	Ser	Trp	Ala	Leu	His	Cys	His	Cys	Ser	Ser
					115				120			125			
Pro	Gly	Ser	Leu	Gln	Cys	Ile	Ala	Gly	Gly	Gln	Val	Leu	Ala	Ser	Trp
					130				135			140			

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Phe Arg Met Val Val Asp Gly Ala Met Phe Asn Gln Arg Phe Ile Trp  
 145 150 155 160  
 Tyr Arg Glu Val Val Asn Tyr Asn Met Pro Lys Glu Val Met Phe Met  
 165 170 175  
 5 Ser Ser Val Phe Met Arg Gly Arg His Leu Ile Tyr Leu Arg Leu Trp  
 180 185 190  
 Tyr Asp Gly His Val Gly Ser Val Val Pro Ala Met Ser Phe Gly Tyr  
 195 200 205  
 Ser Ala Leu His Cys Gly Ile Leu Asn Asn Ile Val Val Leu Cys Cys  
 10 210 215 220  
 Ser Tyr Cys Ala Asp Leu Ser Glu Ile Arg Val Arg Cys Cys Ala Arg  
 225 230 235 240  
 Arg Thr Arg Arg Leu Met Leu Arg Ala Val Arg Ile Ile Ala Glu Glu  
 245 250 255  
 15 Thr Thr Ala Met Leu Tyr Ser Cys Arg Thr Glu Arg Arg Arg Gln Gln  
 260 265 270  
 Phe Ile Arg Ala Leu Leu Gln His His Arg Pro Ile Leu Met His Asp  
 275 280 285  
 Tyr Asp Ser Thr Pro Met  
 290

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTTCTTC CAGCTCTTCC CGCTCTCTCC GTGTGTGACT CGCAGAACGA ATGTGTAGGT	60
TGGCTGGGTG TGCGTTATTG TGCGGTGGTG GATGTTATCA GGGCACGGGC GCATGAAAGGA	120
GTTTACATAG AACCCGAAAGC CAGGGGGCGC CTGGATGCTT TGAGAGAGTG GATATACTAC	180
AACTACTACA CAGAGCGATC TAAGCGCGA GACCGGAGAC GCAGATCTGT TTGTCA CGCC	240
CGCACCTGGT TTGCTCTTCAG GAAATATGAC TAGTCCGGC GTTCCATTG GCATGACACT	300
ACGACCAACA CGATCTCGGT TGCTCTCGGC CACTCCGTAC AGTAG	345

## 35 (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Pro Ala Leu Pro Ala Pro Pro Val Cys Asp Ser Gln Asn	
1 5 10 15	

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Glu Cys Val Gly Trp Leu Gly Val Ala Tyr Ser Ala Val Val Asp Val  
20 25 30  
Ile Arg Ala Ala Ala His Glu Gly Val Tyr Ile Glu Pro Glu Ala Arg  
35 40 45  
5 Gly Arg Leu Asp Ala Leu Arg Glu Trp Ile Tyr Tyr Asn Tyr Tyr Thr  
50 55 60  
Glu Arg Ser Lys Arg Arg Asp Arg Arg Arg Arg Ser Val Cys His Ala  
65 70 75 80  
Arg Thr Trp Phe Cys Phe Arg Lys Tyr Asp Tyr Val Arg Arg Ser Ile  
85 90 95  
10 Trp His Asp Thr Thr Asn Thr Ile Ser Val Val Ser Ala His Ser  
100 105 110  
Val Gln

What is claimed is:

50 55 60  
65 70 75 80  
85 90 95  
100 105 110